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☐ 1: C72368. hypothetical prot...[gi:7437268]

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LOCUS C72368 309 aa linear BCT 21-JUL-2000  
 DEFINITION hypothetical protein TM0509 - Thermotoga maritima (strain MSB8).  
 ACCESSION C72368  
 PID g7437268  
 VERSION C72368 GI:7437268  
 DBSOURCE pir: locus C72368;  
 summary: #length 309 #molecular-weight 34900 #checksum 4927;  
 genetic: #gene TM0509;  
 superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose  
 4-epimerase homology;  
 PIR dates: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change  
 21-Jul-2000.

#### KEYWORDS

SOURCE Thermotoga maritima.

ORGANISM Thermotoga maritima

Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

REFERENCE 1 (residues 1 to 309)

AUTHORS Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J.,  
 Haft, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A.,  
 McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M.,  
 Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A.,  
 Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D.,  
 White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M.

TITLE Evidence for lateral gene transfer between Archaea and bacteria  
 from genome sequence of Thermotoga maritima

JOURNAL Nature 399 (6734), 323-329 (1999)

MEDLINE 99287316

#### FEATURES

Location/Qualifiers

source 1..309

/organism="Thermotoga maritima"

/db\_xref="taxon:2336"

Protein 1..309

/product="hypothetical protein TM0509"

#### ORIGIN

```

1 mnilvtggag figshvvdki iengyqvivv dnlssgkven lnlnalfyeq siedeemmer
61 ifslhrpeyv fhlaaasva isvteparda ktneiigslvl leksikygvk kfifsstgga
121 iygenkvfvp tpeteiphpi spygiakyst emyleffare yglkytvlyr anvygprqdp
181 ygeagvvaif termrlgeev hifgdgeyvr dyvyvddvvr anllamekgd nevfnigtgr
241 gttvnqlfkl lkeitgydke pvykpprkgd vrksildytk akeklgwepk vsleeglklk
301 veyfrktle
  
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Revised: October 24, 2001.

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[\[General\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#)  
[\[Sequence\]](#) [\[Tools\]](#)

## General information about the entry

Entry name	<b>Q9RD76</b>
Primary accession number	<b>Q9RD76</b>
Secondary accession numbers	None
Entered in TrEMBL in	Release 13, May 2000
Sequence was last modified in	Release 13, May 2000
Annotations were last modified in	Release 20, March 2002

## Name and origin of the protein

Protein name	<b>Putative cytochrome P450</b>
Synonyms	None
Gene name	<b>SCF43.12</b>
From	<u>Streptomyces coelicolor</u> [TaxID: 1902]
Taxonomy	<u>Bacteria</u> ; <u>Firmicutes</u> ; <u>Actinobacteria</u> ; <u>Actinobacteridae</u> ; <u>Actinomycetales</u> ; <u>Streptomycineae</u> ; <u>Streptomycetaceae</u> ; <u>Streptomyces</u> .

## References

- [1] SEQUENCE FROM NUCLEIC ACID.  
**STRAIN=A3(2);**  
Saunders D.C., Harris D.;  
 Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.  
**STRAIN=A3(2);**  
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;  
 Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
- [3] SEQUENCE FROM NUCLEIC ACID.  
**STRAIN=A3(2);**  
 MEDLINE=97000351; PubMed=8843436; [NCBI, ExPASy, EBI, Israel, Japan]  
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;  
 "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb *Streptomyces coelicolor* A3(2) chromosome."  
 Mol. Microbiol. 21:77-96(1996).

**Comments**

- ***SIMILARITY:*** BELONGS TO THE CYTOCHROME P450 FAMILY.

**Cross-references**

EMBL	AL136502; CAB66201.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
HSSP	P14779; 1BVY. [ <a href="#">HSSP ENTRY</a> / <a href="#">PDB</a> ]
InterPro	<a href="#">IPR001128</a> ; <a href="#">Cytochrome_P450</a> . <a href="#">IPR000217</a> ; <a href="#">Tubulin</a> . <a href="#">Graphical view of domain structure</a> .
Pfam	<a href="#">PF00067</a> ; <a href="#">p450</a> ; 1.
PRINTS	<a href="#">PR00385</a> ; <a href="#">P450</a> .
PROSITE	<a href="#">PS00086</a> ; <a href="#">CYTOCHROME_P450</a> ; <a href="#">UNKNOWN_1</a> . <a href="#">PS00227</a> ; <a href="#">TUBULIN</a> ; 1.
ProDom	[ <a href="#">Domain structure</a> / <a href="#">List of seq. sharing at least 1 domain</a> ].
ProtoMap	<a href="#">Q9RD76</a> .
PRESAGE	<a href="#">Q9RD76</a> .
ModBase	<a href="#">Q9RD76</a> .
SWISS-2DPAGE	<a href="#">GET REGION ON 2D PAGE</a> .

**Keywords**

**Heme**; **Monooxygenase**; **Oxidoreductase**.

**Features**

None

**Sequence information**

Length: 527 AA	Molecular weight: 57741 Da	CRC64: 4A612C1B7A894780 [This is a checksum on the sequence]
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      |           |           |           |           |           |
MAQTAREPAR DGLPKGFRSA ELGWPELHRI PHPPYRLPLL GDVVGASRRT PMQDSLRYAR
      70           80           90          100          110          120
      |           |           |           |           |           |
RLGPIFRRRA FGKEFVFVWG AALAADLADE ARFAKHVGLG VANLRPVAGD GLFTAYNHEP
      130          140          150          160          170          180
      |           |           |           |           |           |
NWQLAHDVLA PGFSREAMAG YHVMMLDVAA RLTGHWDLAE ASGRAVDVPG DMTKLTLETI
      190          200          210          220          230          240
      |           |           |           |           |           |
ARTGFGHDFG SFERSRLHPF VTAMVGTLG Y AQRLNTVPAP LAPWLLRDAS RRNAADIAHL
      250          260          270          280          290          300
      |           |           |           |           |           |
NRTVDDLVR RRRANGGTGGG TGSGSGSGDL LDRMLETAHP RTGERLSPQN VRRQVITFLV
      310          320          330          340          350          360
      |           |           |           |           |           |
AGHETTSGAL SFALHYLAQH PDVAARARAE VDRVWGDTEA PGYEQVAKLR YVRRVLDESL
      370          380          390          400          410          420
      |           |           |           |           |           |
RLWPTAPGFA REAREDTVLG GTHPMRRGAW ALVLTGMLHR DPEVWGADAE RFDPRFPAK
      430          440          450          460          470          480
      |           |           |           |           |           |
AVRSRAPHTF KPFGTGARAC IGRQFALHEA TLVLGLLLR YELRPEPGYR LRVTERLTLM
      490          500          510          520
      |           |           |           |
PEGLRLHLVR RTAAAPAPGR RTAAPGAADD AGDTVSAAPGC PVHRAGD

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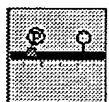
Direct BLAST submission at [NCBI](#)  
(Bethesda, USA)



[ScanProsite](#), [MotifScan](#)



Tools  
Sequence analysis tools: [ProtParam](#),  
[ProtScale](#), [Compute pI/Mw](#), [PeptideMass](#),  
[PeptideCutter](#), [Dotlet \(Java\)](#)



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